ITS2-R: (SEQ ID NO: 6) 5′ ATA TGC TTA AAT TCA GCG GG 3′. The DNA template was of *Stenobrachius leucopsarus* myctophid fish and run for 35 cycles in DNA thermo cycler. (Each cycle consisted of 94°C for 45 Seconds, 48°C for 45 seconds, and 72°C for 1 minute) and hold at 4 degree Centigrade.

On Page 29, delete the paragraph entitled **Example 20**; and replace this paragraph with the following in accordance with 37 CFR §1.121. A marked up version showing changes is attached:

Example 20 :

PCR for confirmation that transformed bacteria has the plasmids with the D-Loop gene inserts.:

PCR amplification using forward and backward D-Loop primers of *Stenobrachius leucopsarus*.

The PCR master mix (100 µl) comprised of Taq Buffer $MgCl_2$ free (10.0 µl), dNTP all the four nucleotides in the ratio of 1:1:1:1 (08.0 µl); D-Loop forward primer 01.0 µl with sequences (PRO-L : 5′ CTA CC 3′), D-Loop backward 01.0 µl, with sequences (D-Loop H: 5′ CCT GAA GTA GGA ACC AGA TG 3′) (SEQ ID NO: 4); $MgCl_2$ (01.0 µl); Taq Polymerase (0.5 µl); and ultrapure water (78.2 µl).

In the Claims:

In accordance with 37 C.F.R. § 1.121, please substitute for original claims 9-19, 29-31, 33-41 and 74-107 the following rewritten version of the same claims, as amended. The changes are shown explicitly in the attached "Version With Markings to Show Changes Made."

9. (Amended) A method as claimed in claim 1 wherein the primer set (forward and backward primers) used for amplification and detection of Cyt b gene contains oligonucleotides with the sequences (SEQ ID NOS 1-2):

CYT 1:	5′	TGA YTT GAA RAA CCA YCG TTG	3′
CYT 2:	5′	CTC CAR TCT TCG RYT TAC AAG	3′

10. (Amended) A method as claimed in claim 1 wherein the primer set (forward and backward primers) used for reamplification and detection of Cyt b gene contains oligonucleotides with the sequences (SEQ ID NOS 3 and 2):

CBI-L: 5′ CCA TCC AAC ATC TCA GCA TGA TGA AA 3′

CYT 2: 5′ CTC CAR TCT TCG RYT TAC AAG 3′

11. (Amended) A method as claimed in claim 1 wherein the primer set (forward and backward primers) used for PCR amplification and detection of D-Loop gene contains oligonucleotides with the sequences :

PRO-L : 5′ CTA CC 3′

D-LOOP H: 5′ CCT GAA GTA GGA ACC AGA TG 3′ (SEQ ID NO: 4)

12. (Amended) A method as claimed in claim 1 wherein the forward and backward primers used for PCR amplification of ITS2 gene were

ITS1 F : 5′ TTG TAC ACA CCGCCCGTC GC 3′ (SEQ ID NO: 41)

ITS2 R : 5′ ATA TGC TTA AAT TCA GCG GG 3′ (SEQ ID NO: 6)

13. (Amended) A method as claimed in claim 1 wherein the forward and backward primers used for PCR reamplification of ITS2 gene from ITS1 F and ITS2 R PCR amplification were

ITS2 F: 5′ CTA CGC CTG TCT GAG TGT C 3′ (SEQ ID NO: 5)

ITS2 R: 5′ ATA TGC TTA AAT TCA GCG GG 3′ (SEQ ID NO: 6)

14. (Amended) A method as claimed in claim 1 wherein the primer set (forward and backward primers) used for PCR amplification of Rhodopsin gene Rod contains oligonucleotides with the sequences (SEQ ID NOS 8 and 7):

ROD-F: 5′ CAT ATG AAT ACC CTC AGT ACT ACC 3′

ROD-R: 5′ TCT TTC CGC AGC ACA ACG TGG 3′

15. (Amended) A method as claimed in claim 1 wherein the primer set (forward and backward primers) used for PCR amplification of 12S RNA gene contains oligonucleotides with the sequences (SEQ ID NOS 9-10):

12 SA-L: 5' AAA CTG GGA TTA GAT ACC CCA CTA T 3'

12 SB-H : 5 ' AGA GTG ACG GGC GGT GTG T 3'

16. (Amended) A method as claimed in claim 1 wherein the primer set (forward and backward primers) used for PCR amplification of 16S RNA gene contains oligonucleotides with the sequences:

16 SAR -L: 5' CGC CTG TTT ATC AAA AAC AT 3' (SEQ ID NO: 11)

16 SBR-H : 5 ' CCG GTC TGA ACT CAG ATC ACG T 3' (SEQ ID NO: 12)

17. (Amended) A method as claimed in claim 1 wherein the forward and backward primers used for PCR amplification of Rhodopsin gene Rod were (SEQ ID NOS 8 and 7:

ROD-F: 5' CAT ATG AAT ACC CTC AGT ACT ACC 3'

ROD-R: 5' TCT TTC CGC AGC ACA ACG TGG 3'

18. (Amended) A method as claimed in claim 1 wherein the primer set (forward and backward primers) used for PCR amplification of 12S RNA gene were (SEQ ID NOS 9-10):

12 SA-L: 5' AAA CTG GGA TTA GAT ACC CCA CTA T 3'

12 SB-H: 5 ' AGA GTG ACG GGC GGT GTG T 3'

19. (Amended) A method as claimed in claim 1 wherein the primer set (forward and backward primers) used for PCR amplification of 16S RNA gene were (SEQ ID NOS 11-12):

16 SAR -L: 5' CGC CTG TTT ATC AAA AAC AT 3'

SBR-H: 5 ' CCG GTC TGA ACT CAG ATC ACG T 3'

29. (Amended) A method claimed in claim 1 wherein the cycle sequencing primer for CYT b gene consisted of oligonucleotides with the sequence:

CYT 1: 5' TGA YTT GAA RAA CCA YCG TTG 3' (SEQ ID NO: 1)

30. (Amended) A method claimed in claim 1 wherein the cycle sequencing primer for CYT b gene consisted of oligonucleotides with the sequence:

CYT 2: 5′ CTC CAR TCT TCG RYT TAC AAG 3′ (SEQ ID NO: 2)

31. (Amended) A method claimed in claim 1 wherein the cycle sequencing primer for CYT b gene consisted of oligonucleotides with the sequence:

CBI-L: 5′ CCA TCC AAC ATC TCA GCA TGA TGA AA 3′ (SEQ ID NO: 3)

33. (Amended) A method claimed in claim 1 wherein the backward cycle sequencing primer for D-Loop region consisted of oligonucleotides with the sequence:

D-LOOP H: 5′ CCT GAA GTA GGA ACC AGA TG 3′ (SEQ ID NO: 4)

34. (Amended) A method as claimed in claim 1 wherein the forward primer used for cycle sequencing of ITS2 gene consisted of oligonucleotides with the sequence:

ITS 1 -F : 5' TTG TAC ACA CCG CCC GTC GC 3' (SEQ ID NO: 41)

35. (Amended) A method as claimed in claim 1 wherein the backward primer used for cycle sequencing of ITS2 gene consisted of oligonucleotides with the sequence:

ITS2 –R : 5′ ATA TGC TTA AAT TCA GCG GG 3′ (SEQ ID NO: 6)

36. (Amended) A method as claimed in claim 1 wherein the forward primer used for cycle sequencing of Rhodopsin gene Rod consisted of oligonucleotides with the sequence:

ROD-F: 5′ CAT ATG AAT ACC CTC AGT ACT ACC 3′ (SEQ ID NO: 8)

37. (Amended) A method as claimed in claim 1 wherein the backward primer used for cycle sequencing consisted of oligonucleotides with the sequence:

ROD-R: 5′ TCT TTC CGC AGC ACA ACG TGG 3′ (SEQ ID NO: 7)

38. (Amended) A method as claimed in claim 1 wherein the forward primer used for cycle sequencing of 12S RNA gene consisted of oligonucleotides with the sequence:

12 SA-L: 5′ AAA CTG GGA TTA GAT ACC CCA CTA T 3′ (SEQ ID NO: 9)

39. (Amended) A method as claimed in claim 1 wherein the backward primer used for cycle sequencing of 12S RNA gene consisted of oligonucleotides with the sequence:

12 SB-H : 5 ' AGA GTG ACG GGC GGT GTG T 3' (SEQ ID NO: 10)

40. (Amended) A method as claimed in claim 1 wherein the forward primer used for cycle sequencing of 16S RNA gene consisted of oligonucleotides with the sequence:

16 SAR -L: 5' CGC CTG TTT ATC AAA AAC AT 3' (SEQ ID NO: 11)

41. (Amended) A method as claimed in claim 1 wherein the backward primer used for cycle sequencing of 16S RNA gene consisted of oligonucleotides with the sequence:

16 SBR-H: 5 ' CCG GTC TGA ACT CAG ATC ACG T 3' (SEQ ID NO: 12)

74. (Amended) The nucleotide base sequences of PSL CYTL (747 bp) comprising (SEQ ID NO: 42):

5'

CTTNCCCATT	TTGGGCGCTT	NGGCNCGCTN	CTCCNCGAGA	CTCTGCGTAN
TAATCCAANT	CNCTNCGGGC	CNCTCCCTAC	CANTNCNCTA	CACCNCAAAT
TNCAACCCNG	TTTCCTCATC	ANTCAACCAC	ATCTGTCGAA	AACNTCAACT
ACGGCTGACT	AATCCGAAAA	CATGCACGCT	AACGGTGCCT	CTTTCTTCTT
CATCTGTATT	TATCTNCNCN	TTGGANGAGG	ACTATNCTAC	GGATCCTACC

TCTACGAAGA GACGTGAGGT GTTGGTGTTA TTCTTCTCCT TCTAATAATG
ATGACTGCNT TTGTTGGCTA TGTGCTNCCC NGAGGACAAA TGTCCTTTTG
AGGTGCTACT GTCATTACAA NCCTACTCTC TGCTGTNCCG TNTGTTNGCG
GCNCTCTANT TCAATGAATT TGAGGTGGCT TCTCCGTAAA CACGCAACGC
TCACTCGTTT CTTCGCNTTC CACTTCTTGT TCCCATTTGT TGTCGCNGCT
ATAACCNNGG TTCACCNGAT TTNCCGACAT CAAACAGGCT CTAAANCCCC
CCCGGNTTGA CTCCATACAA CAAAACCCTC CACCCTATTC NCTATAAAAC
TCTAGGTTCG TGCCCGTATT GGCTTACTTC ATGNCTATTT CCCNGNCGGA
GGGACNAAAA TTCCTGCACC CCCTCCCCNC AAAATAAANA ATGTGTCTNT
CCTACCANAA AACAACNNAN ACGGGGTNTG CNCTTCCATC ATCCACN **3'**

75. (Amended) The nucleotide base sequences of PSLITS2F comprises: (225BP) (SEQ ID NO: 43)

5'

TCTACGATCT ACCGGCNTTT NNTGTGGAAA GACGATCATG
CATTTATGTG TGTCTTTCTA TGGATTTGAA CCGTGTGGTA
CGTCTTTGCG TACTGCTTGG AAGGCTCAAC TTGCTTCTGT
CCTTCTCTTG CAGTCTCGCA CTGTCTATGC AACGTGTTCT
ACTTCGACTT CTGTCGAAAA ATCTTACTTT TGACCTCAGA
TCAGACAAGA CTACCCGCTG AATTT **3'**

76. (Amended) The nucleotide base sequences of PSL PROL comprises: (750 BP) (SEQ ID NO: 44)

5'

CCTTTTCGGN ATAGGCCCAN CTCAAATGAA TTCCTTCTCT
CCTGGTCCAA GCCCAAACTG TGGACGGCAG GTTGACAATG
GTTACAAATC GTGACAAATC GGCTACATAA TTGCCGATAG
CGATGTCGTC AAACCAAGTC AAACAATGGC CGATGTATAT
CGGCCAAACC CATATATGGG TCTGGCTGTA GTTTGTGTTG
AGCAACGTCA CACCAGTGTC TGGTCAGCAT ATAAGATGTT
GACATCTTGC AACATCTTAC CCACAGACAG ACAGTTACGG
CTGCTTACGA ANGGCGCTAG TGTTGTGGTG AGAAACGAAG
ATACATACGT CAAACAGACG CCGGTGCACT TGAAGACACT

GTTTGAAGGT	GCCGCACTAC	TTGACAGACA	GCCCATGATG
CGCTGGACAG	TGACCAAAGC	TACNGGAGGA	CCANATGGAA
ATCCTGTTGG	CGTTGCCGTG	GGACTCAAGT	TGTACACTTT
TGGATGGTTG	ATCACTANAN	CCGCTGCCGG	GAGAAGCACT
CGCTCCTGGT	TCACTAATCA	GATTGAGGTT	AACCANATTG
ANGTAAACAT	CTTCAACACA	GTGTCTTTAT	GCTGGATGAA
ATTNAGCCCA	CNGGACACCA	NAAAAGAATT	NCCNCTGGTT
CTNNCGGGGG	NCCCCNNNAA	CGNNTNTTCC	CCTTNTCTCN
NNNGCGGNGA	AGTTNCCCCC	CCCCACTNAN	NTCTTCCTTC
AANANNTTTC	CNCCNNNAGA	GGTTTTCCCN	3'

77. (Amended) The nucleotide base sequences of ROD PSL SLMB comprises: (748 BP) (SEQ ID NO: 45)

5'

CCTGGTAGGG	TTCCCCGTCA	ACTTCCTCAC	ACTGTACCTC
ACNTTCGAGC	ACAAGAAGCT	ACTAACCCCC	TTAAACTACA
TCCTGCTCAA	CCTGGCGGTC	GGAGACCTCC	TGATGGTGTA
AGGAGGGTTC	ACCACCACCA	TCTACACCTC	CATGCACGGC
TACTTCGTCC	TAGGGAAACT	GGGCTGCGCC	ATCGAAGGTT
TCATGGCCAC	CCATGGTGGT	CAGGTCGCCC	TTTGGTCCCT
GGTGGTTTTG	GCCGTGGAAA	GGTGGCTGGT	CGTCTGCAAN
CCCATCTCCA	GCTTCCGCTT	CCAGGAGTCC	CACTCCCTCA
TGGGCCTGGC	CGTGACCTGG	GTGATGGCGA	CGGCTTGTTC
TGTGCCCCCC	CTGGGTCGGC	TGGTCTCGCT	ACATCCCAGA
AGGCATGCAG	TGCTCATGCG	GAATGGACTA	CTACACTCCC
GCGCCGGGCG	TCAACAATGA	ATCCTACGTN	GTGTACATGT
TCNTCANAAA	AANAATNGGA	CCNCNGGGCG	ATCATNTTGN
TANGNNAAGG	CCAGNTGNTG	NGAGCAGTCA	AGGCGGCCGC
CGCCGCCCAG	CAAGAGTCCG	AGACCACCCA	GAGGGCCGAG
AGGGAAGTCA	CCCGNATGGT	NATNANGATG	GTNATNTCNT
TCNTGGTAAG	NAGGGNGCCA	NACGCCAGCG	TGGCCTGGTG
GATCTTNNGN	AACCAGGGNG	CAGAATTAGG	CCCNGTNTTC

ATGACCCTGC CGGCNTTCTT TGCCAAGA **3'**

78. (Amended) A method as claimed in claim 1 wherein FORWARD (L) primers of CYT b gene region for myctophid fish *Stenobrachius leucopsarus* is an oligonucleotide comprising (SEQ ID NO: 18):

5' CAA CCT CAT CTG TCG TAA AC 3'

and having the following characteristics:

i. is a 20-mer DNA oligonucleotide (sense),

ii. has melting temperature of 56.4 degree celius,

iii. has a molecular weight of 6101.0,

iv. has no hairpin loops,

v. has no single dimers,

vi. has no other dimers,

vii. has no single bulge loops or internal loops, and

viii. has no palindromes.

79. (Amended) A method as claimed in claim 1 wherein BACKWARD (H) primer of CYT b gene region for myctophid fish *Stenobrachius leucopsarus* (SLMB) is an oligonuleotide comprising (SEQ ID NO: 17):

5' GCT CGG GCT GCT GGA ATC TT 3'

and having the following characteristics:

i. is a 20-mer DNA

ii. is an antisense oligonuleotide

iii. has a melting point of 70.8 degree celcius.

iv. has a molecular weight of 6220.1.

v. has no hairpin loops, no single bulge loops, no other internal loops, no single internal loops, no other bulge loops or palindromes.

vi. no single dimers or other dimers.

80. (Amended) A method as claimed in claim 1 wherein forward primer of ITS2 F gene region for myctophid fish *Stenobrachius leucopsarus* (SLMB) is an oligonuleotide comprising (SEQ ID NO: 20):

5' ACT TGA CTG ACC TTC TTA CT 3'

and having the following characteristics:

i. is a 20-mer sense oligonucleotide,

ii. has a melting point of 51.3 degree celcius,

iii. has a molecular weight of 6098.0,

iv. has no palindromes, loops and dimers,

81. (Amended) A method as claimed in claim 1 wherein forward primer of ITS2 H gene region for myctophid fish *Stenobrachius leucopsarus* (SLMB) is an oligonuleotide comprising (SEQ ID NO: 19):

5' ATA CTC TGC GGA CAT ACT TGA CTG 3'

and having the following characteristics:

i. is a 24-mer antisense oligonucleotide,

ii. has a melting point of 65.4 degree celcius.

iii. has a molecular weight of 7407.9.

iv. has no palindromes, loops and dimers.

82. (Amended) A method as claimed in claim 1 wherein forward primer of pro-L for myctophid fish *Stenobrachius leucopsarus* (SLMB) is an oligonuleotide comprising (SEQ ID NO: 21):

5' CAG TCT CGT CAA ACC AAG TCA AAC 3'

and having the following characteristics:

i. is a 24-mer sense oligonucleotide

ii. has a melting point of 67.8 degree celcius.

iii. has a molecular weight of 7354.9.

iv. has no palindromes, loops and dimers.

83. (Amended) A method as claimed in claim 1 wherein backward primer for Dloop for mitochondrial control region (dloop H) gene region for myctophid fish *Stenobrachius leucopsarus* is an oligonuleotide comprising (SEQ ID NO: 22):

5' ATA ATC ATC CAG CAT AAA CAC AC 3'

and having the following characteristics:

i. is a 23-mer antisense oligonucleotide,

ii. has a melting point of 61.2 degree celcius.

iii. has a molecular weight of 7033.7.

iv. has no palindromes, loops and dimers.

84. (Amended) A method as claimed in claim 1 wherein the FORWARD primer (ROD- L) for Rhodopsin gene region of myctophid fish *Stenobrachius leucopsarus* is an oligonucleotide comprising (SEQ ID NO: 23):

5' CCT GGT AGA GTT CGC CGT CA 3'

and having the following characteristics:

i. is a 20-mer sense oligonucleotide

ii. has a melting point of 67.4 degree celcius.

iii. has a molecular weight of 6189.0.

iv. has no palindromes, loops and dimers.

85. (Amended) A method as claimed in claim 1 wherein the backward primer (ROD- H) for Rhodopsin gene region of myctophid fish *Stenobrachius leucopsarus* is an oligonucleotide comprising (SEQ ID NO: 24):

5' CGT GTT CCT TAT CAT TGT GCC T 3'

and having the following characteristics:

i. is a 22-mer antisense oligonucleotide

ii. has a melting point of 66.4 degree celcius.

iii. has a molecular weight of 6738.4.

iv. has no palindromes, loops and dimers.

86. (Amended) A method as claimed in claim 1 wherein the forward primer of 16S-L of the myctophid fish *Lampanyctus regalis* is an oligonucleotide comprising (SEQ ID NO: 26):

5' CAC CAG CCA AGT ATG TTT CTC 3'

and having the following characteristics:

i. is a 21-mer sense oligonucleotide

ii. has a melting point of 61.5 degree celcius.

iii. has a molecular weight of 6421.4.

iv. has no palindromes, loops and dimers.

87. (Amended) A method as claimed in claim 1 wherein the backward primer of 16s rRNA of myctophid fish *Lampanyctus regalis* is an oligonucleotide comprising (SEQ ID NO: 25):

5' TCG TAG TTC AGC AGT CAG 3'

and having the following characteristics:

i. is a 18-mer antisense oligonucleotide

ii. has a melting point of 51.2 degree celcius.

iii. has a molecular weight of 5594.7.

iv. has no palindromes, hairpin loops and dimers.

88. (Amended) A method as claimed in claim 1 wherein the forward primer 16S-L of myctophid fish *Lampanyctus regalis* is an oligonucleotide comprising (SEQ ID NO: 28):

5' CTA TTC GCC TCG CTC AGA C 3'

and having the following characteristics:

i. is a 19-mer sense oligonucleotide

ii. has a melting point of 62.1 degree celcius.

iii. has a molecular weight of 5779.8.

iv. has no palindromes, hairpin loops and dimers.

89. (Amended) A method as claimed in claim 1 wherein a primer 12S-H for *Lampanyctus regalis* (LRMB) is an oligonucleotide comprising (SEQ ID NO: 27):

5' GCC TCC ATC ATC CCT CAC CTT AC 3'

and having the following characteristics:

i. is a 23-mer antisense oligonucleotide

ii. has a melting point of 70.8 degree celcius.

iii. has a molecular weight of 6895.5

iv. has no hairpin loops, dimers, palindromes or bulges and internal loops of either single or other kinds.

90. (Amended) A method as claimed in claim 1 wherein the primer 12S-L for *Lampanyctus regalis* (LRMB) is an oligonucleotide comprising (SEQ ID NO: 28):

5' CTA TTC GCC TCG CTC AGA C 3'

and having the following characteristics:

i. is a 19-mer sense oligonucleotide

ii. has a melting point of 62.1 degree celcius.

iii. has a molecular weight of 5779.8

iv. has no hairpin loops, dimers, palindromes or bulges and internal loops of either single or other kinds.

91. (Amended) A method as claimed in claim 1 wherein 16S-L forward primer for *Diaphus theta* (DTMB) is an oligonucleotide comprising (SEQ ID NO: 30):

5' AAA TCC GCC CTT ATG TGT GTT C 3'

and having the following characteristics:

i. is a 22-mer sense oligonucleotide

ii. has a melting point of 67.9 degree celcius.

iii. has a molecular weight of 6756.4

iv. has no hairpin loops, dimers, palindromes or bulges and internal loops of either single or other kinds.

92. (Amended) A method as claimed in claim 1 wherein 16S-H backward primer for *Diaphus theta* (DTMB) is an oligonucleotide comprising (SEQ ID NO: 29):

5' CTC CGT CCG TCT CGC CTC TG 3'

and having the following characteristics:

i. is a 20-mer antisense oligonucleotide

ii. has a melting point of 71.7 degree celcius.

iii. has a molecular weight of 6052.0

iv. has no hairpin loops, dimers, palindromes or bulges and internal loops of either single or other kinds.

93. (Amended) A method as claimed in claim 1 wherein 12S-H forward primer for *Diaphus theta* (DTMB) is an oligonucleotide comprising (SEQ ID NO: 31):

5' CAT CGG CTT GCT CTA TTC CTT G 3'

and having the following characteristics:

i. is a 22-mer antisense oligonucleotide

ii. has a melting point of 68.8 degree celcius.

iii. has a molecular weight of 6723.4

iv. has no hairpin loops, dimers, palindromes or bulges and internal loops of either single or other kinds.

94. (Amended) A method as claimed in claim 1 wherein 12S-L forward primer for *Diaphus theta* (DTMB) is an oligonucleotide comprising (SEQ ID NO: 32):

5' TCT ATC GGC GGC GTA TCA C 3'

and having the following characteristics:

i. is a 19-mer sense oligonucleotide

ii. has a melting point of 65.8 degree celcius.

iii. has a molecular weight of 5859.8

iv. has no hairpin loops, dimers, palindromes or bulges and internal loops of either single or other kinds.

95. (Amended) A method as claimed in claim 1 wherein 16S-H primer for *Tarletonbeania crenularis* (TCMB) is an oligonucleotide comprising (SEQ ID NO: 33):

5' GGC GAT TCT ACG GCA CGG GCG 3'

and having the following characteristics:

i. is a 21-mer antisense oligonucleotide

ii. has a melting point of 80.4 degree celcius.

iii. has a molecular weight of 6568.3

iv. has no hairpin loops, dimers, palindromes or bulges and internal loops of either single or other kinds.

96. (Amended) A method as claimed in claim 1 wherein 16S-L forward primer for *Tarletonbeania crenularis* (TCMB) is an oligonucleotide comprising (SEQ ID NO: 34):

5' AAA CTG GTC CTC AAC TAT GTC A 3'

and having the following characteristics:

i. is a 22-mer sense oligonucleotide

ii. has a melting point of 60.7 degree celcius.

iii. has a molecular weight of 6758.5

iv. has no hairpin loops, dimers, palindromes or bulges and internal loops of either single or other kinds.

97. (Amended) A method as claimed in claim 1 wherein 16S-H backward primer for *Tarletonbeania crenularis* (TCMB) is an oligonucleotide comprising (SEQ ID NO: 33):

5' GGC GAT TCT ACG GCA CGG GCG 3'

and having the following characteristics:

i. is a 21-mer antisense oligonucleotide

ii. has a melting point of 80.4 degree celcius.

iii. has a molecular weight of 6568.3

iv. has no hairpin loops, dimers, palindromes or bulges and internal loops of either single or other kinds.

98. (Amended) A method as claimed in claim 1 wherein 12S-H backward primer for *Tarletonbeania crenularis* (TCMB) is an oligonucleotide comprising (SEQ ID NO: 35):

5' CCG ATT CAG CCA CGA TTC CCT C 3'

and having the following characteristics:

i. is a 22-mer antisense oligonucleotide

ii. has a melting point of 74.6 degree celcius.

iii. has a molecular weight of 6671.4

iv. has no hairpin loops, dimers, palindromes or bulges and internal loops of either single or other kinds.

99. (Amended) A method as claimed in claim 1 wherein 12S-L forward primer for *Tarletonbeania crenularis* (TCMB) is an oligonucleotide comprising (SEQ ID NO: 42):

5' CCT AAA GCC CAG ATA ACT ACA 3'

i. is a 21-mer sense oligonucleotide

ii. has a melting point of 59.2 degree celcius.

iii. has a molecular weight of 6432.3

iv. has no hairpin loops, dimers, palindromes or bulges and internal loops of either single or other kinds.

100. (Amended) A method as claimed in claim 1 wherein 16S-H backward primer for *Protomyctophum crockeri* (PCMB) is an oligonucleotide comprising (SEQ ID NO: 37):

5' CGT GTT CTG ATG ATG ATG TGC T 3'

i. is a 22-mer antisense oligonucleotide

ii. has a melting point of 64.7 degree celcius.

iii. has a molecular weight of 6867.5

iv. has no hairpin loops, dimers, palindromes or bulges and internal loops of either single or other kinds.

101. (Amended) A method as claimed in claim 1 wherein 16S-L forward primer for *Protomyctophum crockeri* (PCMB) is an oligonucleotide comprising (SEQ ID NO: 38):

5' ATT CCT TCC TCT TAG TAT G 3'

i. is a 19-mer sense oligonucleotide

ii. has a melting point of 49.5 degree celcius.

iii. has a molecular weight of 5799.8

iv. has no hairpin loops, dimers, palindromes or bulges and internal loops of either single or other kinds.

102. (Amended) A method as claimed in claim 1 wherein 12S-H backward primer for *Protomyctophum crockeri* (PCMB) is an oligonucleotide comprising (SEQ ID NO: 39):

5' GCT GAA CTT ACT ATG CCC TAC T 3'

i. is a 22-mer antisense oligonucleotide

ii. has a melting point of 60.3 degree celcius.

iii. has a molecular weight of 6725.4

iv. has no hairpin loops, dimers, palindromes or bulges and internal loops of either single or other kinds.

103. (Amended) A method as claimed in claim 1 wherein 12S-L forward primer for *Protomyctophum crockeri* (PCMB) is an oligonucleotide comprising (SEQ ID NO: 40):

5' CCG ATT GAC GCC GAA CTA TG 3'

i. is a 20-mer sense oligonucleotide

ii. has a melting point of 68.1 degree celcius.

iii. has a molecular weight of 6182.1

iv. has no hairpin loops, dimers, palindromes or bulges and internal loops of either single or other kinds.

104. (Amended) A method as claimed in claim 1 wherein 16S-H backward primer for *Stenobrachius leucopsarus* (SLMB) is an oligonucleotide comprising (SEQ ID NO: 15):

5' TAC GCA TAA CGG CTC TGG 3'

i. is a 18-mer DNA oligonucleotide (Antisense)

ii. has a melting point of 61.4 degree celcius.

iii. has a molecular weight of 5579.7

iv. has no hairpin loops, dimers, palindromes or bulges and internal loops of either single or other kinds.

105. (Amended) A method as claimed in claim 1 wherein 16S-L forward primer for *Stenobrachius leucopsarus* (SLMB) is an oligonucleotide comprising (SEQ ID NO: 16):

5' CTA CTA CAC CTC AAC TAC ATC T 3'

i. is a 22-mer sense oligonucleotide

ii. has a melting point of 52.4 degree celcius.

iii. has a molecular weight of 6638.4

iv. has no hairpin loops, dimers, palindromes or bulges and internal loops of either single or other kinds.

106. (Amended) A method as claimed in claim 1 wherein 12S-H forward primer for *Stenobrachius leucopsarus* (SLMB) is an oligonucleotide comprising (SEQ ID NO: 13):

5' CCC ACT CAC TGC TAA CTC C 3'

i. is a 19-mer sense oligonucleotide

ii. has a melting point of 58.4 degree celcius.

iii. has a molecular weight of 5708.8

iv. has no hairpin loops, dimers, palindromes or bulges and internal loops of either single or other kinds.

107. (Amended) A method as claimed in claim 1 wherein 12S-L forward primer for *Stenobrachius leucopsarus* (SLMB) is an oligonucleotide comprising (SEQ ID NO: 14:

5' GGC TAA CTA CAA TCA TCT GCT 3'

i. is a 21-mer sense oligonucleotide

ii. has a melting point of 58.5 degree celcius.

iii. has a molecular weight of 6445.2

iv. has no hairpin loops, dimers, palindromes or bulges and internal loops of either single or other kinds.